

OIKE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/002,854

DATE: 12/13/2001

TIME: 10:27:57

Input Set : A:\M07657038.txt

Output Set: N:\CRF3\12132001\I002854.raw

Does Not Comply
Corrected Diskette Needed

4 <110> APPLICANT: Scadden, David T.
 5 Poznansky, Mark C.
 6 Olszak, Ivona T.
 7 Brown, Edward M.
 9 <120> TITLE OF INVENTION: THE CaR RECEPTOR AS A MEDIATOR OF
 10 MIGRATORY CELL CHEMOTAXIS AND/OR CHEMOKINESIS
 13 <130> FILE REFERENCE: M0765/7038/ERG/KA
 C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/002,854
 C--> 15 <141> CURRENT FILING DATE: 2001-11-01
 15 <150> PRIOR APPLICATION NUMBER: PCT/US00/15440
 16 <151> PRIOR FILING DATE: 2000-06-02
 18 <160> NUMBER OF SEQ ID NOS: 2
 20 <170> SOFTWARE: FastSEQ for Windows Version 3.0

ERRORED SEQUENCES

308 <210> SEQ ID NO: 2
 309 <211> LENGTH: 1078
 310 <212> TYPE: PRT
 311 <213> ORGANISM: Homo sapiens
 313 <220> FEATURE:
 314 <221> NAME/KEY: PEPTIDE
 315 <222> LOCATION: (1)...(1078)
 316 <223> OTHER INFORMATION: Ca-sensing Receptor
 318 <400> SEQUENCE: 2
 319 Met Ala Phe Tyr Ser Cys Cys Trp Val Leu Leu Ala Leu Thr Trp His
 320 1 5 10 15
 321 Thr Ser Ala Tyr Gly Pro Asp Gln Arg Ala Gln Lys Lys Gly Asp Ile
 322 20 25 30
 323 Ile Leu Gly Gly Leu Phe Pro Ile His Phe Gly Val Ala Ala Lys Asp
 324 35 40 45
 325 Gln Asp Leu Lys Ser Arg Pro Glu Ser Val Glu Cys Ile Arg Tyr Asn
 326 50 55 60
 327 Phe Arg Gly Phe Arg Trp Leu Gln Ala Met Ile Phe Ala Ile Glu Glu
 328 65 70 75 80
 329 Ile Asn Ser Ser Pro Ala Leu Leu Pro Asn Leu Thr Leu Gly Tyr Arg
 330 85 90 95
 331 Ile Phe Asp Thr Cys Asn Thr Val Ser Lys Ala Leu Glu Ala Thr Leu
 332 100 105 110
 333 Ser Phe Val Ala Gln Asn Lys Ile Asp Ser Leu Asn Leu Asp Glu Phe
 334 115 120 125
 335 Cys Asn Cys Ser Glu His Ile Pro Ser Thr Ile Ala Val Val Gly Ala
 336 130 135 140
 337 Thr Gly Ser Gly Val Ser Thr Ala Val Ala Asn Leu Leu Gly Leu Phe
 338 145 150 155 160
 339 Tyr Ile Pro Gln Val Ser Tyr Ala Ser Ser Ser Arg Leu Leu Ser Asn

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```

340          165          170          175
341  Lys Asn Gln Phe Lys Ser Phe Leu Arg Thr Ile Pro Asn Asp Glu His
342          180          185          190
343  Gln Ala Thr Ala Met Ala Asp Ile Ile Glu Tyr Phe Arg Trp Asn Trp
344          195          200          205
345  Val Gly Thr Ile Ala Ala Asp Asp Tyr Gly Arg Pro Gly Ile Glu
346          210          215          220
347  Lys Phe Arg Glu Glu Ala Glu Glu Arg Asp Ile Cys Ile Asp Phe Ser
348          225          230          235          240
349  Glu Leu Ile Ser Gln Tyr Ser Asp Glu Glu Glu Ile Gln His Val Val
350          245          250          255
351  Glu Val Ile Gln Asn Ser Thr Ala Lys Val Ile Val Val Phe Ser Ser
352          260          265          270
353  Gly Pro Asp Leu Glu Pro Leu Ile Lys Glu Ile Val Arg Arg Asn Ile
354          275          280          285
355  Thr Gly Lys Ile Trp Leu Ala Ser Glu Ala Trp Ala Ser Ser Ser Leu
356          290          295          300
357  Ile Ala Met Pro Gln Tyr Phe His Val Val Gly Gly Thr Ile Gly Phe
358          305          310          315          320
359  Ala Leu Lys Ala Gly Gln Ile Pro Gly Phe Arg Glu Phe Leu Lys Lys
360          325          330          335
361  Val His Pro Arg Lys Ser Val His Asn Gly Phe Ala Lys Glu Phe Trp
362          340          345          350
363  Glu Glu Thr Phe Asn Cys His Leu Gln Glu Gly Ala Lys Gly Pro Leu
364          355          360          365
365  Pro Val Asp Thr Phe Leu Arg Gly His Glu Glu Ser Gly Asp Arg Phe
366          370          375          380
367  Ser Asn Ser Ser Thr Ala Phe Arg Pro Leu Cys Thr Gly Asp Glu Asn
368          385          390          395          400
369  Ile Ser Ser Val Glu Thr Pro Tyr Ile Asp Tyr Thr His Leu Arg Ile
370          405          410          415
371  Ser Tyr Asn Val Tyr Leu Ala Val Tyr Ser Ile Ala His Ala Leu Gln
372          420          425          430
373  Asp Ile Tyr Thr Cys Leu Pro Gly Arg Gly Leu Phe Thr Asn Gly Ser
374          435          440          445
375  Cys Ala Asp Ile Lys Lys Val Glu Ala Trp Gln Val Leu Lys His Leu
376          450          455          460
377  Arg His Leu Asn Phe Thr Asn Asn Met Gly Glu Gln Val Thr Phe Asp
378          465          470          475          480
379  Glu Cys Gly Asp Leu Val Gly Asn Tyr Ser Ile Ile Asn Trp His Leu
380          485          490          495
381  Ser Pro Glu Asp Gly Ser Ile Val Phe Lys Glu Val Gly Tyr Tyr Asn
382          500          505          510
383  Val Tyr Ala Lys Lys Gly Glu Arg Leu Phe Ile Asn Glu Glu Lys Ile
384          515          520          525
385  Leu Trp Ser Gly Phe Ser Arg Glu Val Pro Phe Ser Asn Cys Ser Arg
386          530          535          540
387  Asp Cys Leu Ala Gly Thr Arg Lys Gly Ile Ile Glu Gly Glu Pro Thr
388          545          550          555          560

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```

389  Cys Cys Phe Glu Cys Val Glu Cys Pro Asp Gly Glu Tyr Ser Asp Glu
390              565              570              575
391  Thr Asp Ala Ser Ala Cys Asn Lys Cys Pro Asp Asp Phe Trp Ser Asn
392              580              585              590
393  Glu Asn His Thr Ser Cys Ile Ala Lys Glu Ile Glu Phe Leu Ser Trp
394              595              600              605
395  Thr Glu Pro Phe Gly Ile Ala Leu Thr Leu Phe Ala Val Leu Gly Ile
396              610              615              620
397  Phe Leu Thr Ala Phe Val Leu Gly Val Phe Ile Lys Phe Arg Asn Thr
398              625              630              635              640
399  Pro Ile Val Lys Ala Thr Asn Arg Glu Leu Ser Tyr Leu Leu Leu Phe
400              645              650              655
401  Ser Leu Leu Cys Cys Phe Ser Ser Ser Leu Phe Phe Ile Gly Glu Pro
402              660              665              670
403  Gln Asp Trp Thr Cys Arg Leu Arg Gln Pro Ala Phe Gly Ile Ser Phe
404              675              680              685
405  Val Leu Cys Ile Ser Cys Ile Leu Val Lys Thr Asn Arg Val Leu Leu
406              690              695              700
407  Val Phe Glu Ala Lys Ile Pro Thr Ser Phe His Arg Lys Trp Trp Gly
408              705              710              715              720
409  Leu Asn Leu Gln Phe Leu Leu Val Phe Leu Cys Thr Phe Met Gln Ile
410              725              730              735
411  Val Ile Cys Val Ile Trp Leu Tyr Thr Ala Pro Pro Ser Ser Tyr Arg
412              740              745              750
413  Asn Gln Glu Leu Glu Asp Glu Ile Ile Phe Ile Thr Cys His Glu Gly
414              755              760              765
415  Ser Leu Met Ala Leu Gly Phe Leu Ile Gly Tyr Thr Cys Leu Leu Ala
416              770              775              780
417  Ala Ile Cys Phe Phe Phe Ala Phe Lys Ser Arg Lys Leu Pro Glu Asn
418              785              790              795              800
419  Phe Asn Glu Ala Lys Phe Ile Thr Phe Ser Met Leu Ile Phe Phe Ile
420              805              810              815
421  Val Trp Ile Ser Phe Ile Pro Ala Tyr Ala Ser Thr Tyr Gly Lys Phe
422              820              825              830
423  Val Ser Ala Val Glu Val Ile Ala Ile Leu Ala Ala Ser Phe Gly Leu
424              835              840              845
425  Leu Ala Cys Ile Phe Phe Asn Lys Thr Tyr Ile Ile Leu Phe Lys Pro
426              850              855              860
427  Ser Arg Asn Thr Ile Glu Glu Val Arg Cys Ser Thr Ala Arg His Ala
428              865              870              875              880
429  Phe Lys Val Ala Ala Arg Ala Thr Leu Arg Arg Ser Asn Val Ser Arg
430              885              890              895
431  Lys Arg Ser Ser Ser Leu Gly Gly Ser Thr Gly Ser Thr Pro Ser Ser
432              900              905              910
433  Ser Ile Ser Ser Lys Ser Asn Ser Glu Asp Pro Phe Pro Gln Pro Glu
434              915              920              925
435  Arg Gln Lys Gln Gln Gln Pro Leu Ala Leu Thr Gln Gln Glu Gln Gln
436              930              935              940
437  Gln Gln Pro Leu Thr Leu Pro Gln Gln Gln Arg Ser Gln Gln Gln Pro

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```

438 945          950          955          960
439 Arg Cys Lys Gln Lys Val Ile Phe Gly Ser Gly Thr Val Thr Phe Ser
440          965          970          975
441 Leu Ser Phe Asp Glu Pro Gln Lys Asn Ala Met Ala His Arg Asn Ser
442          980          985          990
443 Thr His Gln Asn Ser Leu Glu Ala Gln Lys Ser Ser Asp Thr Leu Thr
444          995          1000          1005
445 Arg His Gln Pro Leu Leu Pro Leu Gln Cys Gly Glu Thr Asp Leu Asp
446          1010          1015          1020
447 Leu Thr Val Gln Glu Thr Gly Leu Gln Gly Pro Val Gly Gly Asp Gln
E--> 448 1025          1030          1035          1040 1040
449 Arg Pro Glu Val Glu Asp Pro Glu Glu Leu Ser Pro Ala Leu Val Val
450          1045          1050          1055
451 Ser Ser Ser Gln Ser Phe Val Ile Ser Gly Gly Gly Ser Thr Val Thr
452          1060          1065          1070
453 Glu Asn Val Val Asn Ser
454          1075

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/002,854

DATE: 12/13/2001

TIME: 10:27:58

Input Set : A:\M07657038.txt

Output Set: N:\CRF3\12132001\I002854.raw

L:15 M:270 C: Current Application Number differs, Replaced Current Application No

L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:303 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1

L:448 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2